```
1     AGATGAGTGT GGGCGTCGA AGAGTCAAGT TGCTGGGCAT
        METSerVal GlyArgArg ArgValLysLeu LeuGlyIl
41    CCTGATGATG GCAAATGTCT TCATTTATTT GATTGTGGAA
      eLeuMETMET AlaAsnValPhe IleTyrLeu IleValGlu
81    GTCTCCAAAA ACAGTAGCCA AGACAAAAAT GGAAAGGGAG
      ValSerLysAsn SerSerGln AspLysAsn GlyLysGlyG
121   GAGTAATAAT CCCGAAAGAG AAGTTCTGGA AGCCACCCAG
      lyValIleIle ProLysGlu LysPheTrpLys ProProSe
161   CACTCCCCGG GCATACTGGA ACAGGGAACA GGAGAAGCTG
      rThrProArg AlaTyrTrpAsn ArgGluGln GluLysLeu
201   AACAGGTGGT ACAATCCCAT CTTGAACAGG GTGGCCAATC
      AsnArgTrpTyr AsnProIle LeuAsnArg ValAlaAsnG
241   AGACAGGGGA GCTAGCCACA TCTCCAAACA CAAGTCACCT
      lnThrGlyGlu LeuAlaThr SerProAsnThr SerHisLe
281   GAGCTATTGT GAACCAGACT CGACGGTCAT GACAGCTGTG
      uSerTyrCys GluProAspSer ThrValMET ThrAlaVal
321   ACAGATTTTA ATAATCTGCC GGACAGATTT AAAGACTTTC
      ThrAspPheAsn AsnLeuPro AspArgPhe LysAspPheL
361   TCTTGTATTT GAGATGCCGG AATTACTCGC TGCTTATAGA
      euLeuTyrLeu ArgCysArg AsnTyrSerLeu LeuIleAs
401   TCAACCGAAG AAATGTGCAA AGAAGCCCTT CTTACTATTG
      pGlnProLys LysCysAlaLys LysProPhe LeuLeuLeu
441   GCGATAAAGT CCCTCATTCC ACATTTTGCC AGAAGGCAAG
      AlaIleLysSer LeuIlePro HisPheAla ArgArgGlnA
481   CAATTCGGGA GTCTTGGGGC CGAGAAACCA ACGTAGGGAA
      laIleArgGlu SerTrpGly ArgGluThrAsn ValGlyAs
521   CCAGACAGTA GTGAGGGTCT TCCTGTTGGG CAAGACACCC
      nGlnThrVal ValArgValPhe LeuLeuGly LysThrPro
561   CCAGAGGACA ACCACCCTGA CCTTTCGGAC ATGCTTAAGT
      ProGluAspAsn HisProAsp LeuSerAsp METLeuLysP
601   TTGAGAGTGA CAAGCACCAG GACATCCTCA TGTGGAACTA
      heGluSerAsp LysHisGln AspIleLeuMET TrpAsnTy
641   TAGAGACACA TTCTTCAACC TGTCCCTGAA GGAAGTGCTG
      rArgAspThr PhePheAsnLeu SerLeuLys GluValLeu
```

FIG. 1A

```
681  TTTCTTAGGT GGGTGAGCAC TTCCTGTCCA GACGCAGAGT
     PheLeuArgTrp ValSerThr SerCysPro AspAlaGluP
721  TTGTCTTCAA GGGCGATGAT GACGTGTTTG TGAACACCCA
     heValPheLys GlyAspAsp AspValPheVal AsnThrHi
761  TCACATCCTT AATTACTTGA ATAGCTTATC CAAGAGCAAA
     sHisIleLeu AsnTyrLeuAsn SerLeuSer LysSerLys
801  GCCAAAGACT TGTTCATAGG TGACGTGATC CACAATGCTG
     AlaLysAspLeu PheIleGly AspValIle HisAsnAlaG
841  GGCCTCACCG GGATAAGAAA CTGAAGTACT ACATCCCAGA
     lyProHisArg AspLysLys LeuLysTyrTyr IleProGl
881  AGTCTTCTAC ACCGGCGTCT ACCCACCGTA TGCCGGGGGT
     uValPheTyr ThrGlyValTyr ProProTyr AlaGlyGly
921  GGTGGATTCC TGTACTCCGG CCCCCTTGCC TTGAGGCTGT
     GlyGlyPheLeu TyrSerGly ProLeuAla LeuArgLeuT
961  ACAGTGCGAC TAGCCCGGTC CATCTCTACC CTATTGATGA
     yrSerAlaThr SerArgVal HisLeuTyrPro IleAspAs
1001 TGTTTATACG GGAATGTGCC TTCAGAAACT GGGCCTTGTT
     pValTyrThr GlyMETCysLeu GlnLysLeu GlyLeuVal
1041 CCAGAGAAGC ACAAAGGCTT CAGGACATTT GATATTGAAG
     ProGluLysHis LysGlyPhe ArgThrPhe AspIleGluG
1081 AGAAAAATAA GAAAAATATT TGTTCCTATA TAGACCTAAT
     luLysAsnLys LysAsnIle CysSerTyrIle AspLeuME
1121 GTTAGTACAT AGCAGAAAAC CTCAAGAGAT GATTGATATC
     TLeuValHis SerArgLysPro GlnGluMET IleAspIle
1161 TGGTCTCAGT TGCAAAGTCC TAATTTAAAA TGCTGA
     TrpSerGlnLeu GlnSerPro AsnLeuLys Cys
```

FIG. 1B

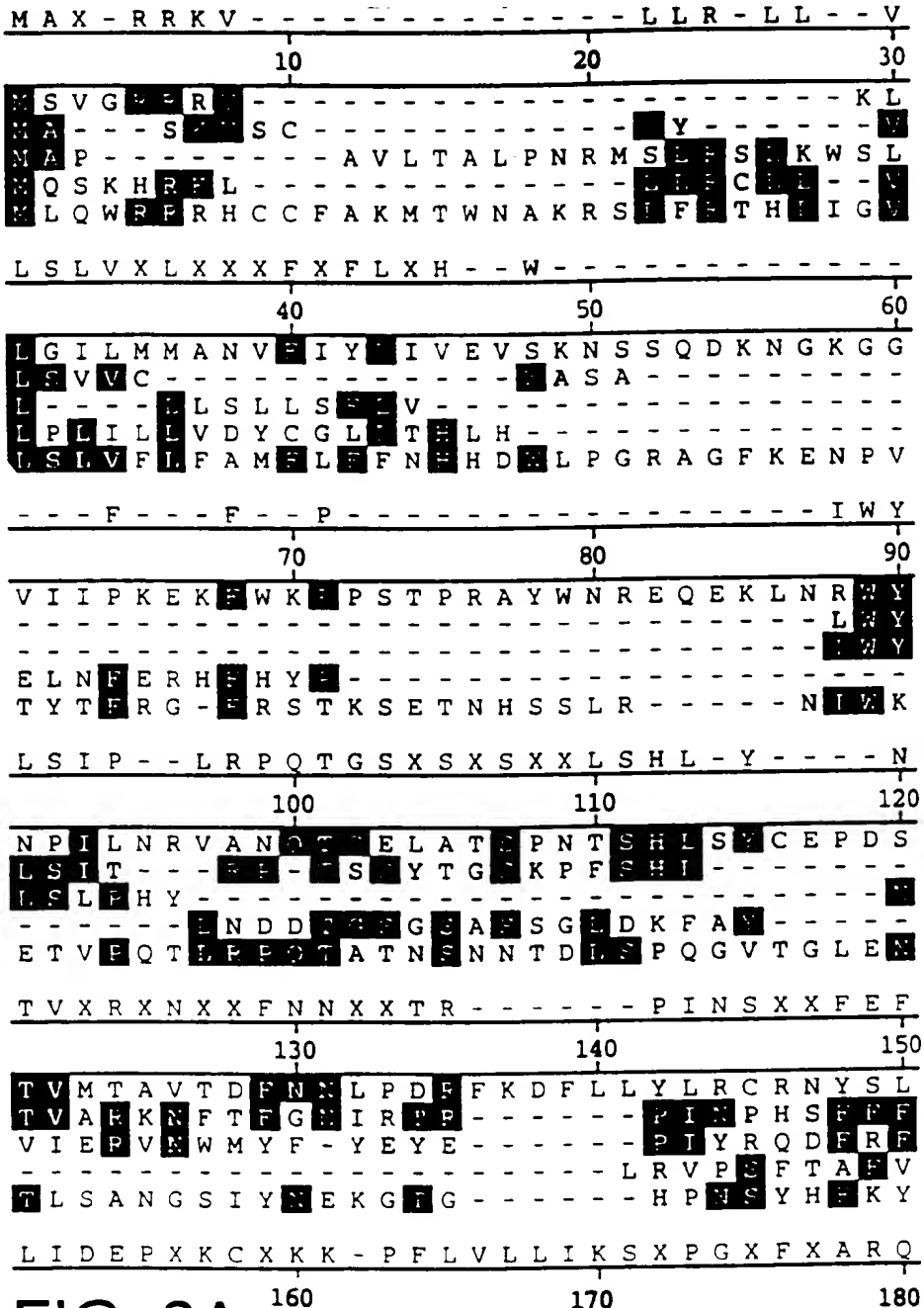

FIG. 2A

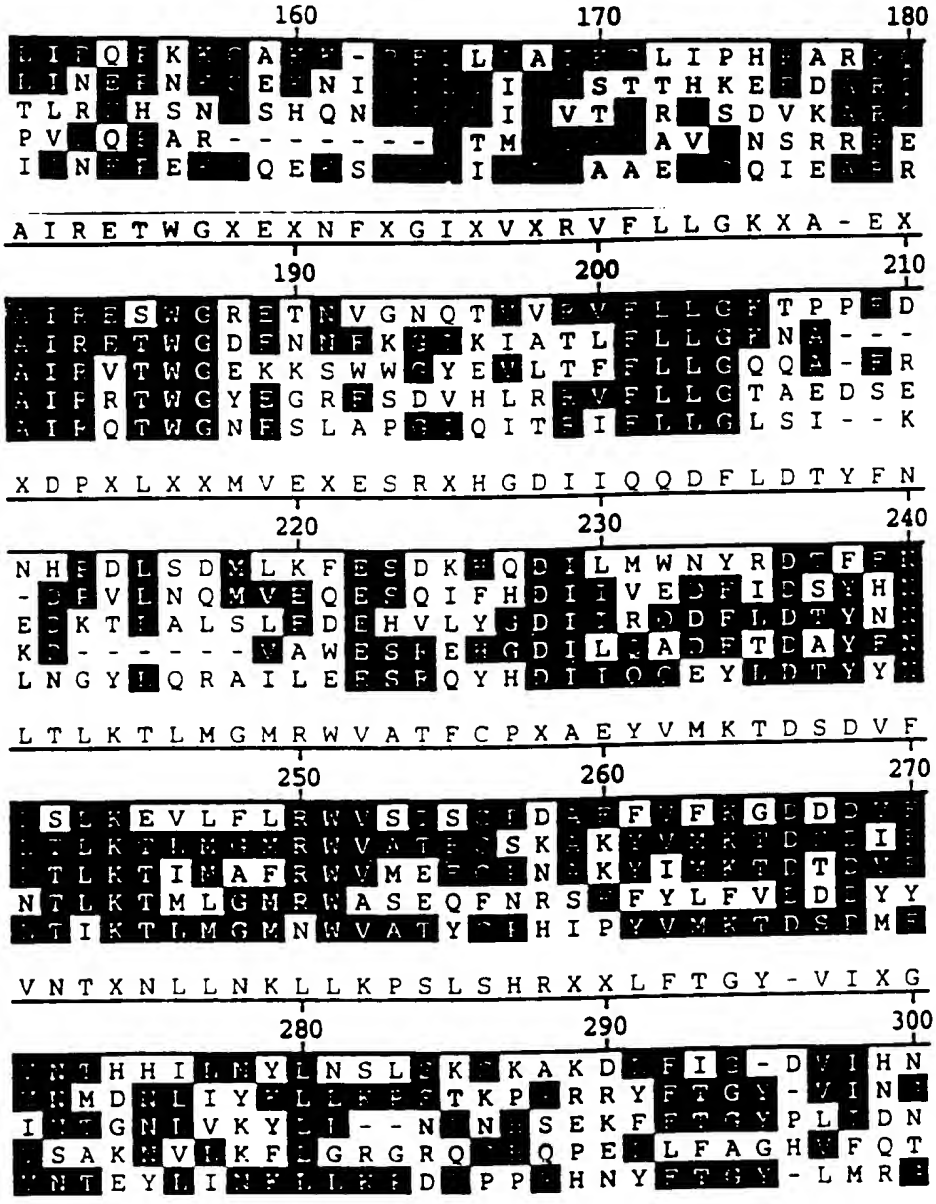

FIG. 2B

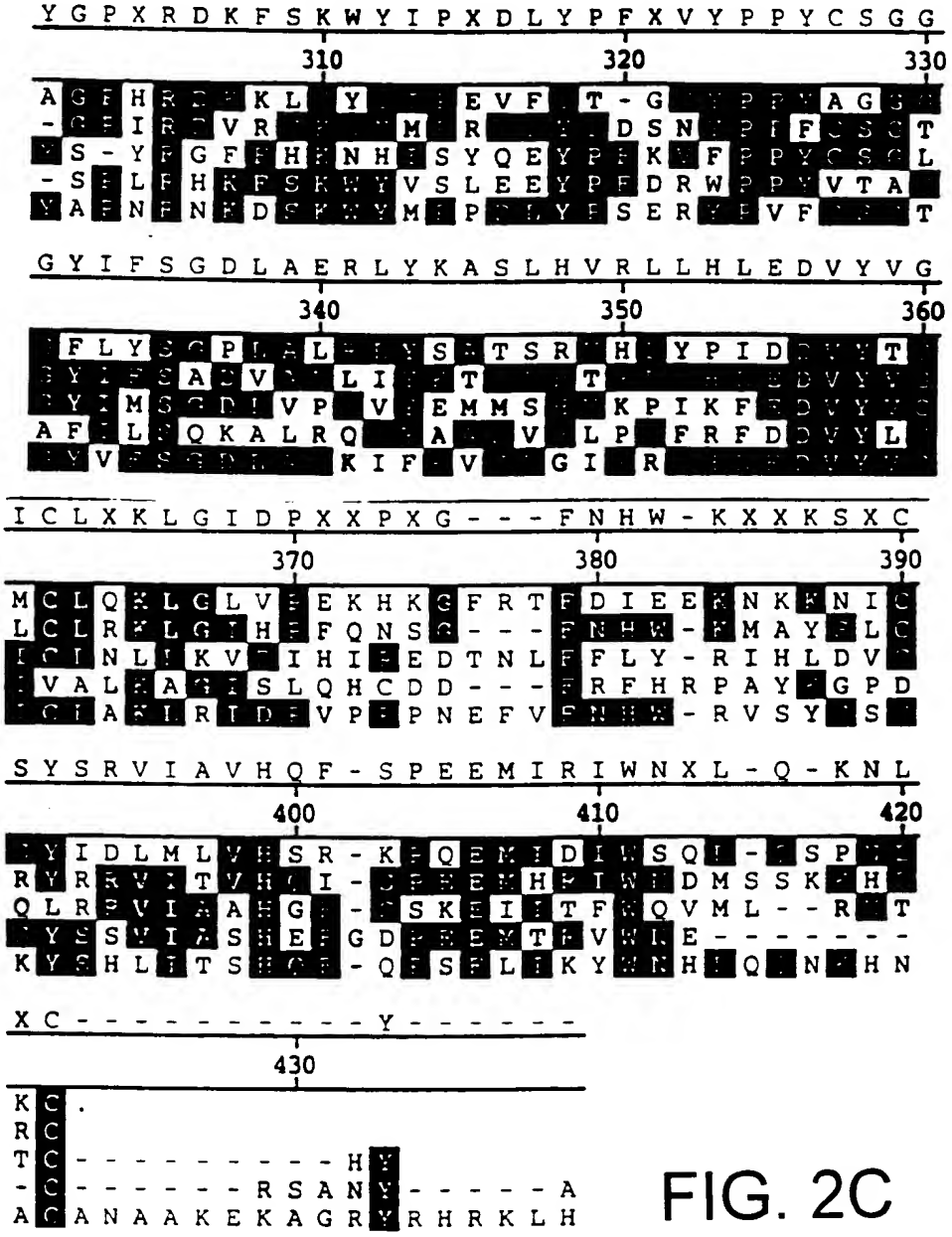

FIG. 2C

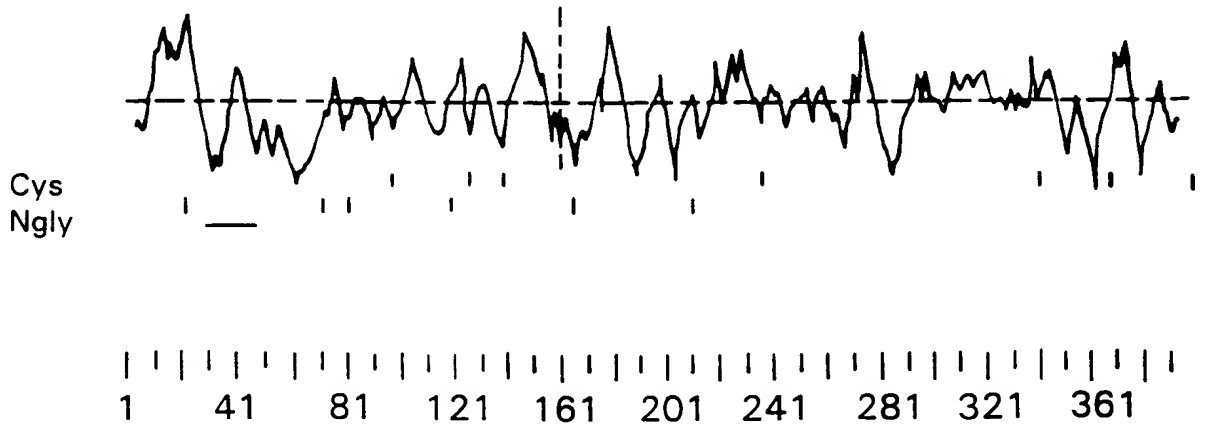

FIG. 3

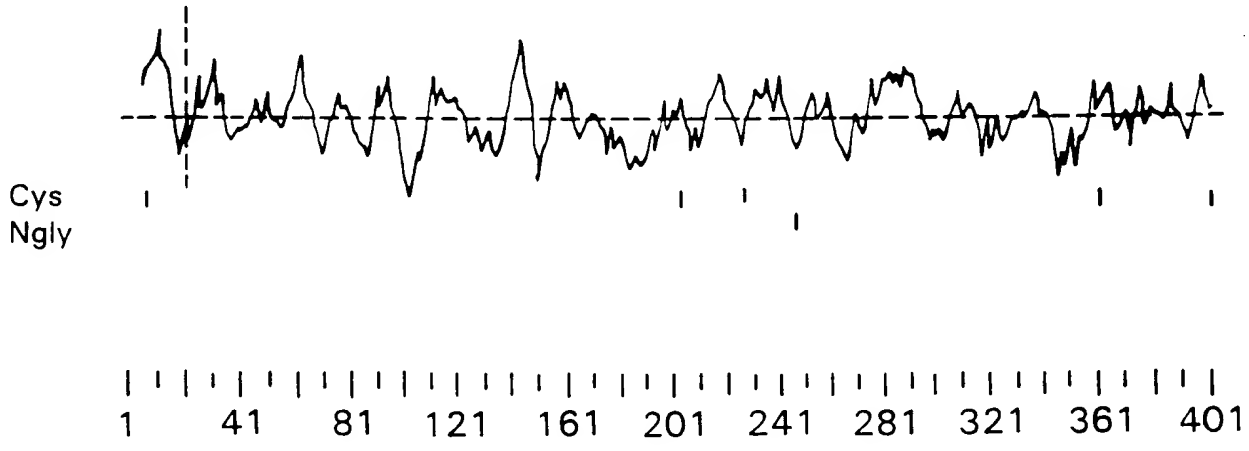

FIG. 5

```
1     ATGATTTGCC CTTCAGCTTT ACTGGTTATT TTAAGAAATT
      METIleCysPro SerAlaLeu LeuValIle LeuArgAsnL
41    TAATACGGGA AGAAAAAATC ATTTCTCAAG AGATCCTCAA
      euIleArgGlu GluLysIle IleSerGlnGlu IleLeuAs
81    TTTGATTGAA TTAAGGATGA AAAAAGGGAA TATTCAGTTG
      nLeuIleGlu LeuArgMETLys LysGlyAsn IleGlnLeu
121   ACAAACTCTG CAATCAGTGA TGCATTAAAA GAAATCGATA
      ThrAsnSerAla IleSerAsp AlaLeuLys GluIleAspS
161   GTAGTGTGCT CAATGTTGCT GTCACCGGGG AGACGGGATC
      erSerValLeu AsnValAla ValThrGlyGlu ThrGlySe
201   AGGGAAGTCC AGCTTCATCA ATACCCTGAG AGGCATTGGG
      rGlyLysSer SerPheIleAsn ThrLeuArg GlyIleGly
241   AATGAAGAAG AAGGTGCAGC TAAAACTGGG GTGGTGGAGG
      AsnGluGluGlu GlyAlaAla LysThrGly ValValGluV
281   TAACCATGGA AAGACATCCA TACAAACACC CCAATATACC
      alThrMETGlu ArgHisPro TyrLysHisPro AsnIlePr
321   CAATGTGGTT TTTTGGGACC TGCCTGGGAT TGGAAGCACA
      oAsnValVal PheTrpAspLeu ProGlyIle GlySerThr
361   AATTTCCCAC CAAACACTTA CCTGGAGAAA ATGAAGTTCT
      AsnPheProPro AsnThrTyr LeuGluLys METLysPheT
401   ATGAGTACGA TTTCTTCATT ATTATTTCGG CCACAGGCTT
      yrGluTyrAsp PhePheIle IleIleSerAla ThrArgPh
441   CAAGAAAAAT GATATAGACA TTGCCAAAGC AATCAGCATG
      eLysLysAsn AspIleAspIle AlaLysAla IleSerMET
481   ATGAAGAAGG AATTCTACTT CGTGAGAACC AAGGTGGACT
      METLysLysGlu PheTyrPhe ValArgThr LysValAspS
521   CTGACATAAC AAATGAAGCA GATGGCAAAC CTCAAACCTT
      erAspIleThr AsnGluAla AspGlyLysPro GlnThrPh
561   TGACAAAGAA AAGGTCCTGC AGGACATCCG CCTTAACTGT
      eAspLysGlu LysValLeuGln AspIleArg LeuAsnCys
601   GTGAACACCT TTAGGGAGAA TGGCATTGCT GAGCCACCAA
      ValAsnThrPhe ArgGluAsn GlyIleAla GluProProI
641   TCTTCCTGCT CTCTAACAAA AATGTTTGTC ACTATGACTT
      lePheLeuLeu SerAsnLys AsnValCysHis TyrAspPh
```

FIG. 4A

```
681  CCCCGTCCTG ATGGACAAGC TGATAAGTGA CCTCCCTATC
     eProValLeu METAspLysLeu IleSerAsp LeuProIle
721  TACAGGAGAC ACAATTTTAT GGTCTCCTTA CCCAATATCA
     TyrArgArgHis AsnPheMET ValSerLeu ProAsnIleT
761  CAGATTCAGT CATTGAAAAG AAGCGGCAAT TTCTGAAGCA
     hrAspSerVal IleGluLys LysArgGlnPhe LeuLysGl
801  RAGGATTTGG CTGGAAGGAT TTGCTGCTGA CCTAGTGAAT
     nArgIleTrp LeuGluGlyPhe AlaAlaAsp LeuValAsn
841  ATCATCCCTT CTCTGACCTT TCTCTTGGAC AGTGATTTGG
     IleIleProSer LeuThrPhe LeuLeuAsp SerAspLeuG
881  AGACTCTGAA GAAAAGCATG AAATTCTACC GCACTGTGTT
     luThrLeuLys LysSerMET LysPheTyrArg ThrValPh
921  TGGAGTGGAT GAAACATCTT TGCAGAGATT AGCTAGGGAC
     eGlyValAsp GluThrSerLeu GlnArgLeu AlaArgAsp
961  TGGGAAATAG AGGTGGATCA GGTGGAGGCC ATGATAAAAT
     TrpGluIleGlu ValAspGln ValGluAla METIleLysS
1001 CTCCTGCTGT GTTCAAACCT ACAGATGAAG AAACAATACA
     erProAlaVal PheLysPro ThrAspGluGlu ThrIleGl
1041 AGAAAGGCTT TCAAGATATA TTCAGGAGTT CTGTTTGGCT
     nGluArgLeu SerArgTyrIle GlnGluPhe CysLeuAla
1081 AATGGGTACT TACTTCCTAA AAATAGTTTT CTTAAAGAAA
     AsnGlyTyrLeu LeuProLys AsnSerPhe LeuLysGluI
1121 TATTTTACCT GAAATATTAT TTCCTTGACA TGGTGACTGA
     lePheTyrLeu LysTyrTyr PheLeuAspMET ValThrGl
1161 GGATGCTAAA ACTCTTCTTA AAGAGATATG TTTAAGAAAC
     uAspAlaLys ThrLeuLeuLys GluIleCys LeuArgAsn
1201 TAG
```

FIG. 4B

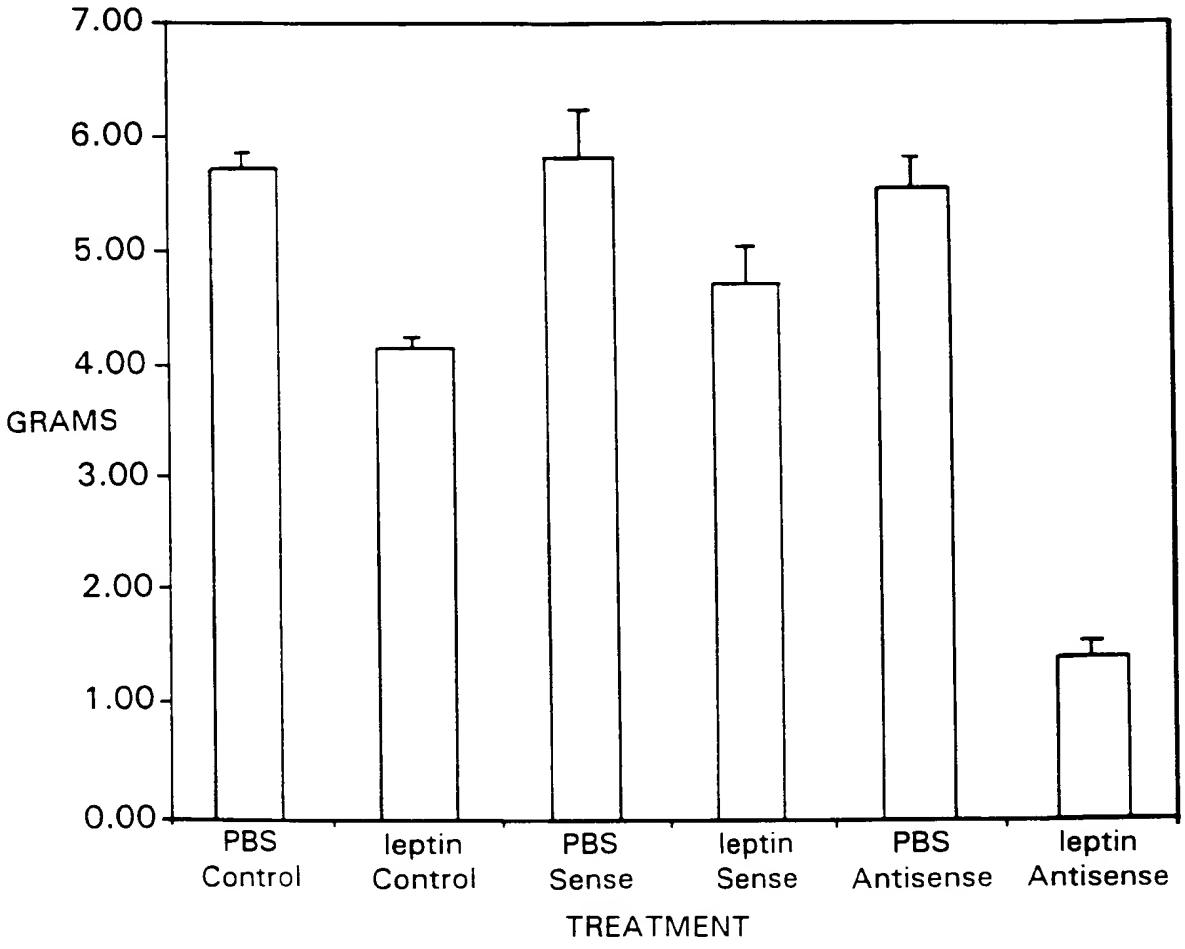

FIG. 6

5'

ACGCGTCCGCGCAGCGGCAGCGGCAGCAGCGGCAACAAGTGCCGGAGGCTA
GCAGAGCCAAGCCGGAGCAGTCCCTGCCGCCGACACCGCCGGGCCGCCCGTC
CGGGGCGCCGCGCATGGAGCGTGAGCTGCGGCGGTCGCCGGGCTGAGCCGC
GCGGAGCGGCCGGGACGTGGATGTGGCCGCGATCTCCCGCCCTTGCCCCCGC
CCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAA**ATG**AGTGTTGGA
CGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTA
TTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAAAATGGAAAAGGG
GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGG
CATACTGGAACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCT
GAGCATGCTGACCAACCAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAG
CCATCTGAACTACTGCGAACCTGACCTGAGGGTCACGTCGGTGGTTACGGGT
TTTAACAACTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGCCG
CAATTATTCACTGCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCT
TGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAAGCAATC
CGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGA
GTCTTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAG
ATATGCTGAAATTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTA
CAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGG
TAAGTACTTCCTGCCCAGACACTGAGTTTGTTTTCAAGGGCGATGACGATGTT
TTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACCAA
AGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGG
GATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCC
ACCCTATGCAGGGGGAGGGGGGTTCCTCTACTCCGGCCACCTGGCCCTGAGG
CTGTACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATAC
TGGAATGTGCCTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTC

FIG. 7A

AGGACATTTGATATCGAGGAGAAAAACAAAAATAACATCTGCTCCTATGTAG
ATCTGATGTTAGTACATAGTAGAAAACCTCAAGAGATGATTGATATTTGGTCT
CAGTTGCAGAGTGCTCATTTAAAATGCTAAAATAGATACAAACTCAATTTKG
SATWGRAAGGGGTWTTTTGRATWGGYCCCATGTTGGGGTCTCACATTAGAGT
AATTTCTATTTNAANCATGAAATTGCCTTTATGAGTGATACCCATTTANGGCC
TCTAANCCTTCATTTGNACTCACGTGAAGAAGGGAAAGCGGGAGAAGGTAAT
TTNTTTATGGTGAATGGCAGGATATTGGTCTGACTTACCGNTAGGGGANTTTA
AAACTGGNCCTTTTTGAATCTGTTTGGATGGCCCTT

FIG. 7B

MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPE
AYWNREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFN
NLPDRFKDFLLYLRCRNYSLLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWG
QESNAGNQTVVRVFLLGQTPPEDNHPDLSDMLKFESEKHQDILMWNYRDTFFNL
SLKEVLFLRWVSTSCPDTEFVFKGDDDVFVNTHHILNYLNSLSKTKAKDLFIGDV
IHNAGPHRDKKLKYYIPEVVYSGLYPPYAGGGGFLYSGHLALRLYHITDQVHLY
PIDDVYTGMCLQKLGLVPEKHKGFRTFDIEEKNKNNICSYVDLMLVHSRKPQEM
IDIWSQLQSAHLKC

FIG. 8

```
246 ATGAGTGTTGGACGTCGAAGAATAAAGTTGTTG--GG-TATCCTGATGATGGCAAATGTC 302
    ||||||||||||||||||||||||||||||||  || ||||||||||||||||||||||
  1 ATGAGTGTTGGACGTCGAAGAATAAAGTTGTTGTTGGGTATCCTGATGATGGCAAATGTC 60

303 TTCATTTATTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAAATGGAAAAGGG 362
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 TTCATTTATTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAAATGGAAAAGGG 120

363 GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGG 422
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGG 180

423 AACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAAC 482
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 AACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAAC 240

483 CAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGAC 542
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 CAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGAC 300

543 CTGAGGGTCACGTCGGTGGTTACGGGTTTTAACAACTTGCCGGACAGATTTAAAGACTTT 602
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 CTGAGGGTCACGTCGGTGGTTACGGGTTTTAACAACTTGCCGGACAGATTTAAAGACTTT 360

603 CTGCTGTATTTGAGATGCCGCAATTATTCACTGCTTATAGATCAGCCGGATAAGTGTGCA 662
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 CTGCTGTATTTGAGATGCCGCAATTATTCACTGCTTATAGATCAGCCGGATAAGTGTGCA 420

663 AAGAAACCTTTCTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAA 722
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 AAGAAACCTTTCTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAA 480

723 GCAATCCGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTC 782
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GCAATCCGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTC 540

783 TTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAGATATGCTGAAA 842
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

FIG. 9A

```
541 TTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAGATATGCTGAAA 600

843 TTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTACAGAGACACTTTCTTCAAC 902
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 TTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTACAGAGACACTTTCTTCAAC 660

903 TTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAG 962
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 TTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAG 720

963 TTTGTTTTCAAGGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTG 1022
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 TTTGTTTTCAAGGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTG 780

1023 AATAGTTTATCCAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCT 1082
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781  AATAGTTTATCCAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCT 840

1083 GGACCTCATCGGGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTC 1142
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841  GGACCTCATCGGGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTC 900

1143 TACCCACCCTATGCAGGGGGAGGGGGGTTCCTCTACTCCGGCCACCTGGCCCTGAGGCTG 1202
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901  TACCCACCCTATGCAGGGGGAGGGGGGTTCCTCTACTCCGGCCACCTGGCCCTGAGGCTG 960

1203 TACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATACTGGAATGTGC 1262
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
961  TACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATACTGGAATGTGC 1020

1263 CTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAG 1322
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 CTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAG 1080

1323 GAGAAAAACAAAAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAA 1382
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 GAGAAAAACAAAAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAA 1140

1383 CCTCAAGAGATGATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAAATGCTAA 1439
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1141 CCTCAAGAGATGATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAAATGCTAA 1197
```

FIG. 9B

MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN
MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN
MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN

REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL
REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL
REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL

LYLRCRNYSLLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF
LYLRCRNYSLLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF
LYLRCRNYSLLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF

LLGQTPPEDNHPDLSDMLKFESEKHQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDTEF
LLGQTPPEDNHPDLSDMLKFESEKHQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDTEF
LLGQTPPEDNHPDLSDMLKFESEKHQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDTEF

VFKGDDDVFVNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLKYYIPEVVYSGLY
VFKGDDDVFVNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLKYYIPEVVYSGLY
VFKGDDDVFVNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLKYYIPEVVYSGLY

PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTGMCLQKLGLVPEKHKGFRTFDIEE
PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTGMCLQKLGLVPEKHKGFRTFDIEE
PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTGMCLQKLGLVPEKHKGFRTFDIEE

KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC
KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC
KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC

FIG. 10

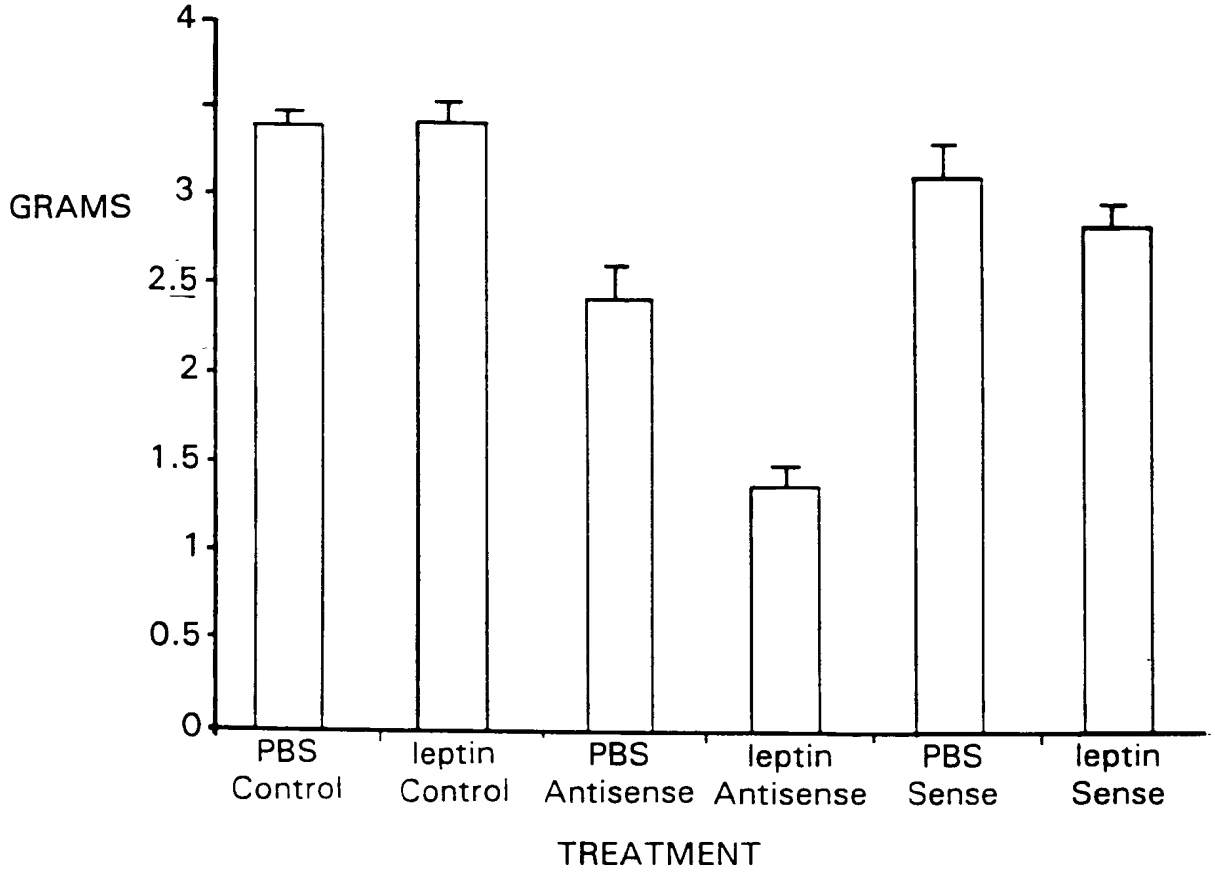

FIG. 11